



OIIPE

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/771,208

DATE: 03/13/2002

TIME: 14:31:43

Input Set : A:\407T-923710US.txt

Output Set: N:\CRF3\03132002\I771208.raw

3 <110> APPLICANT: MEDRANO, JUAN
 4 BRADFORD, ERIC
 5 HORVAT, SIMON
 7 <120> TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
 9 <130> FILE REFERENCE: 407T-923710US
 11 <140> CURRENT APPLICATION NUMBER: US 09/771,208
 12 <141> CURRENT FILING DATE: 2001-01-26
 14 <150> PRIOR APPLICATION NUMBER: US 08/999,477
 15 <151> PRIOR FILING DATE: 1997-12-29
 17 <160> NUMBER OF SEQ ID NOS: 20
 19 <170> SOFTWARE: PatentIn version 3.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1667
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Mus musculus
 26 <400> SEQUENCE: 1

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31	ggaagccaga	gacaagcagg	tactccgctc	cctgcgtctg	gagctgggtg	ccgaggtact	180
33	ggtggaagga	ctggttcttc	agtaccttta	ccaggaagga	atlttgacag	aaaaccacat	240
35	tcaagaaatc	aaagctcaaa	ccacaggcct	ccggaagaca	atgctgttgc	tggacatcct	300
37	gccttccagg	ggccccaag	cttttgacac	cttccctgat	tccctccagg	aatttccctg	360
39	ggtaagagag	aagctggaga	aggcgagaga	ggaagtctca	gccgagctgc	ctacaggtga	420
41	ctggatggcc	ggaatccccct	cacacatcct	cagcagctcg	ccatcagacc	agcagattaa	480
43	ccagctggct	cagaggetag	gcccggagtg	ggagcccgtg	gtcctgtctc	tgggactgtc	540
45	ccagaccgac	atctaccgct	gcaaggccaa	ccatccccac	aacgtgcatt	cgcaggtggt	600
47	ggaggccttt	gtccgctggc	gccagcgttt	tgggaagcag	gccaccttcc	taagcttaca	660
49	caagggcctc	caggcaatgg	aggctgatcc	ctccctgctc	cagcacatgc	tggagtgacc	720
51	tgaccccccc	ccgcgcccc	ccccacttg	ctgtgggggt	ggtggggcgt	gggttcccaa	780
53	gtcacactgg	ctgaaccgga	cttttctcag	caggtggcct	tgttctgggc	ttttcagtga	840
55	tctgtttacg	gaaagagatc	gtccaccact	cactcaacca	tcgattggct	tttaattgctt	900
57	gaagactgcg	ctgttgtaac	tatggtttgg	aactttgtgg	ctggccttta	acaggaggcc	960
59	agaaaaaaca	caacaccac	cctacccaac	cccccaaaa	atcatgctac	agcatcgaat	1020
61	gcaggtgtcc	tgcatacaag	gcagctacac	ttgtgttgcc	tggagactgg	attgtgcatt	1080
63	tagctcttca	taatggtgat	gataataaaa	aagcaaattg	tgatatagaa	tgtgcctctt	1140
65	tcaatgagag	agtattatat	cacacacaca	cacacacaca	cacacacaca	tacacacaca	1200
67	cacaccaatc	ttctgttgca	tagacggagg	gtgtaaaaat	atgggagtg	agcaagattg	1260
69	atagcagtca	tgtgacgacg	gagataaata	actcaggcag	gatgtataga	tttaagcatga	1320
71	gacaccgaag	ctccctgcag	aggccaggga	gagaacggaa	gaccttcac	tttaacaaatt	1380
73	gtatgaggag	tctctgtcca	tttgttaaag	gcattggatc	agagacaaga	gggctcagtg	1440
75	tttctcttga	ggcctgaatg	gctgaaggcg	gtgagttccc	gaggggcgtc	atgggttgct	1500
77	cagcctttca	tttaactgcac	atagtgttag	ccagacaggt	gtacgtgttt	gtcatcccat	1560
79	ctaagagact	gaagcaggag	gatcacctgt	acatgactgc	ttctttcaac	attttaaaaat	1620

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81 gtgtaacttc tattaaattc tctcagtgca aaaaaaaaaa aaaaaaa      1667
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85 <211> LENGTH: 304
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87 <213> ORGANISM: Mus musculus
89 <400> SEQUENCE: 2
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92 gaggtactgg tggaaggact ggttcttcag tacctttacc aggaaggaat ttgacagaa      120
94 aaccacattc aacaaatcaa agctcaaacc acaggcctcc ggaagacaat gctgttgctg      180
96 gacatcctgc cttccagggg ccccaaagct ttgacacct tctcgaattc cctccaggaa      240
98 ttccctggg taagagagaa gctggagaag gcgagagagg aagtctcagc cgagctgcct      300
100 acag      304
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104 <211> LENGTH: 160
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106 <213> ORGANISM: bovine sp
108 <400> SEQUENCE: 3
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111 ggtactggtg gaggggctag tctccagta tctttatcag gaaggggtct tgacagaaag      120
113 ccacgttcaa gaaattaaag ctcaagccac aggcctccgg      160
116 <210> SEQ ID NO: 4
117 <211> LENGTH: 539
118 <212> TYPE: PRT
119 <213> ORGANISM: Mus musculus
121 <400> SEQUENCE: 4
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124 1 5 10 15
126 Ser Gly Leu Asn Val Ala Leu Leu Glu Ala Arg Gly Ser Glu Arg Leu
127 20 25 30
129 Glu Ala Arg Gly Leu Glu Gly Leu Leu Glu Gly Leu Tyr Ala Leu Ala
130 35 40 45
132 Gly Leu Val Ala Leu Leu Glu Val Ala Leu Gly Leu Gly Leu Tyr Leu
133 50 55 60
135 Glu Val Ala Leu Leu Glu Gly Leu Asn Thr Tyr Arg Leu Glu Thr Tyr
136 65 70 75 80
138 Arg Gly Leu Asn Gly Leu Gly Leu Tyr Ile Leu Glu Leu Glu Thr His
139 85 90 95
141 Arg Gly Leu Ala Ser Asn His Ile Ser Ile Leu Glu Gly Leu Asn Gly
142 100 105 110
144 Leu Ile Leu Glu Leu Tyr Ser Ala Leu Ala Gly Leu Asn Thr His Arg
145 115 120 125
147 Thr His Arg Gly Leu Tyr Leu Glu Ala Arg Gly Leu Tyr Ser Thr His
148 130 135 140
150 Arg Met Glu Thr Leu Glu Leu Glu Leu Glu Ala Ser Pro Ile Leu Glu
151 145 150 155 160
153 Leu Glu Pro Arg Ser Glu Arg Ala Arg Gly Gly Leu Tyr Pro Arg Leu
154 165 170 175
156 Tyr Ser Ala Leu Ala Pro His Glu Ala Ser Pro Thr His Arg Pro His
157 180 185 190

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159 Glu Leu Glu Ala Ser Pro Ser Glu Arg Leu Glu Gly Leu Asn Gly Leu
 160 195 200 205
 162 Pro His Glu Pro Arg Thr Arg Pro Val Ala Leu Ala Arg Gly Gly Leu
 163 210 215 220
 165 Leu Tyr Ser Leu Glu Gly Leu Leu Tyr Ser Ala Leu Ala Ala Arg Gly
 166 225 230 235 240
 168 Gly Leu Gly Leu Val Ala Leu Ser Glu Arg Ala Leu Ala Gly Leu Leu
 169 245 250 255
 171 Glu Pro Arg Thr His Arg Gly Leu Tyr Ala Ser Pro Thr Arg Pro Met
 172 260 265 270
 174 Glu Thr Ala Leu Ala Gly Leu Tyr Ile Leu Glu Pro Arg Ser Glu Arg
 175 275 280 285
 177 His Ile Ser Ile Leu Glu Leu Glu Ser Glu Arg Ser Glu Arg Ser Glu
 178 290 295 300
 180 Arg Pro Arg Ser Glu Arg Ala Ser Pro Gly Leu Asn Gly Leu Asn Ile
 181 305 310 315 320
 183 Leu Glu Ala Ser Asn Gly Leu Asn Leu Glu Ala Leu Ala Gly Leu Asn
 184 325 330 335
 186 Ala Arg Gly Leu Glu Gly Leu Tyr Pro Arg Gly Leu Thr Arg Pro Gly
 187 340 345 350
 189 Leu Pro Arg Val Ala Leu Val Ala Leu Leu Glu Ser Glu Arg Leu Glu
 190 355 360 365
 192 Gly Leu Tyr Leu Glu Ser Glu Arg Gly Leu Asn Thr His Arg Ala Ser
 193 370 375 380
 195 Pro Ile Leu Glu Thr Tyr Arg Ala Arg Gly Cys Tyr Ser Leu Tyr Ser
 196 385 390 395 400
 198 Ala Leu Ala Ala Ser Asn His Ile Ser Pro Arg His Ile Ser Ala Ser
 199 405 410 415
 201 Asn Val Ala Leu His Ile Ser Ser Glu Arg Gly Leu Asn Val Ala Leu
 202 420 425 430
 204 Val Ala Leu Gly Leu Ala Leu Ala Pro His Glu Val Ala Leu Ala Arg
 205 435 440 445
 207 Gly Thr Arg Pro Ala Arg Gly Gly Leu Asn Ala Arg Gly Pro His Glu
 208 450 455 460
 210 Gly Leu Tyr Leu Tyr Ser Gly Leu Asn Ala Leu Ala Thr His Arg Pro
 211 465 470 475 480
 213 His Glu Leu Glu Ser Glu Arg Leu Glu His Ile Ser Leu Tyr Ser Gly
 214 485 490 495
 216 Leu Tyr Leu Glu Gly Leu Asn Ala Leu Ala Met Glu Thr Gly Leu Ala
 217 500 505 510
 219 Leu Ala Ala Ser Pro Pro Arg Ser Glu Arg Leu Glu Leu Glu Gly Leu
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 222 Asn His Ile Ser Met Glu Thr Leu Glu Gly Leu
 223 530 535
 225 <210> SEQ ID NO: 5
 226 <211> LENGTH: 20
 227 <212> TYPE: DNA
 C--> 228 <213> ORGANISM: Artificial
 230 <220> FEATURE:

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Input Set : A:\407T-923710US.txt

Output Set: N:\CRF3\03132002\I771208.raw

231 <223> OTHER INFORMATION: PCR primer
 233 <400> SEQUENCE: 5
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 239 <212> TYPE: DNA
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 242 <220> FEATURE:
 243 <223> OTHER INFORMATION: PCR primer
 245 <400> SEQUENCE: 6
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 249 <210> SEQ ID NO: 7
 250 <211> LENGTH: 22
 251 <212> TYPE: DNA
 C--> 252 <213> ORGANISM: Artificial
 254 <220> FEATURE:
 255 <223> OTHER INFORMATION: PCR primer
 257 <400> SEQUENCE: 7
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 261 <210> SEQ ID NO: 8
 262 <211> LENGTH: 21
 263 <212> TYPE: DNA
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 266 <220> FEATURE:
 267 <223> OTHER INFORMATION: PCR primer
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 274 <211> LENGTH: 13908
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 276 <213> ORGANISM: Mus musculus
 278 <400> SEQUENCE: 9
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 281 aaaacacatg ctatggtttg aatggaaaaa tatcccatga aggcttatgt atttgagtca 120
 283 cttcttagct ggtagcactc acttttgaag gctgtaaagc cttcaatctg tgggtcctac 180
 285 ccctttggca aacottgatc tccaaagtta cataagcaca ggcacacact tccacttcct 240
 287 ctgaggtttt ctaccaagaa aggatcaacc attcataaaa tgttggtcct agtgaaccct 300
 289 gcacattgta gaggcttaaa aagtttaatt tgggcctcca actcactaca caggaaactcc 360
 291 agcgggatcc gcctgtccgt tcatgctaac ctttcaccga catcttgttt ttaagtttac 420
 293 agaaaacggt agggacctaa agaaggatcat tacattacag tacattacag tacaacagaa 480
 295 gttacaaagt agcaatgagg ggcttgggga tttagctcag tgctagagcg cttgcctagc 540
 297 aagtgcaaga ccctaggttc ggtcctcagc tctgaaaaat caaaacaaaa caaaacaaag 600
 299 tagcaatgat aataatttta tgggtgaggg gtcacatga tatgaggaaac tgtattaaac 660
 301 ggtcgctgca ttagggagga tgaggaccac tgtggggctc agctgaagga agtgagttgc 720
 303 tgggtgtaggg caccggagtg ctatagtgtaa accggtttcc tgtctccctt ctaaggctga 780
 305 ctgcaccact aattcctgcc tcccgtggag ggtgctttcc aggctccaag ccttcctgcc 840
 307 atgtttggaat gtgtcctgtg aacctatgaac cgagatcaat ctttcctccc ttccatcacc 900
 309 tctgccaggt ggtttggtca tagtactcag tagagtaagg aggctggaag atttactaca 960
 311 cctgacaaaag aaaaattaat ctgtatgatc tcaaaaaaaaa aaaaaaaaaa aacaccacca 1020

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Input Set : A:\407T-923710US.txt

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313 ccaacaacaa aaaaaccaac aaaaaaccaa aaccctttag gagtgcagaa gcacaggcac 1080

315 acacttccac ttctcttgag gttttctacc aagaaaggat caaccattca taaaacgttg 1140

317 gtcttagtta tccctgcaca ttgttagaggc ttaaaaagtt taacttgggc ctccaactca 1200

319 ctacacagaa ctccagaggg atccgcctgt ccgttcatgc taacctttca ccgacatctt 1260

321 gtttttaagt ttacagaaaa cgttagggac ctaaagaagg taagcctcct gctaagttac 1320

323 tccctggcct tacacaggct ttctaaaaact tgagtaagag gcctccttcc catcaaagat 1380

325 tccaggaaaa cagcctcccc cctccgcggc cacacatacg aatctatcgc tgacaaagcc 1440

327 cctgtaagct ggcttatgtc ctccctcgcg gttcaccatt ctgtaagtgc atagaattat 1500

329 ttaagaggaa aaaaattact gtggataaaa attgggttcgg ggccttgga ttggccggtc 1560

331 gtgttggtt tcttccagg gccggcaggc ggggcaccag gcaaggcttg gaagccgcgc 1620

333 ctctctcaac ctctcctggc cacccttgcc caacttcccc atagacacag cttcaactaa 1680

335 aagtggccat tgacctttca agcttttgag cagtggggca acagaacagt atttcaaaga 1740

337 aaaatggtta tcgaaatttc gaatccggtt ttcccatgag tgtttttttt ttgttttgtt 1800

339 tttctgttaa aaaaaaaaaa agtaggtcac attcaaagtg ggtcacgttt caggagccgg 1860

341 cgtgcctgga tgccggcgcg gaggttaggt ggctctttac agagtgggag gtgagggtcc 1920

343 caataggaaa gaagtactgg gatcaatacg aactccgggt ccttggtttt gcaaggattc 1980

345 acagagacaa acgcaccagg cctgtgacct cgcacccac ccgggcacag gtaaggcac 2040

347 ctctctgta ggggtggccg ggtgggtctc ccgaagggca agcaggagt gagctgagga 2100

349 ggaaaggaga agctgggcaa ggtgatgca ggggactacc agttggagct ccagggggga 2160

351 gggattgagg gcagctctgc cagctttaag gaggcgtca gctcgtctct ttcttggcct 2220

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363 agacacaggg gcaggtactg gtggcttaat aggcattggc tggggacttc tcttgttcc 2580

365 cgagcaccgc gaggtgcagg gtcagaggag ggcggagtcg caggcttcca cccgcagcc 2640

367 accagcacca gcacccgcac cggctctctc caccggctc ccttgaagcc tgcgcattag 2700

369 cggccggggc ctctttaaag cgttgccggg ggtgcggtc acgtgaggcg gattcctgga 2760

371 aagttcctgg aaagcggcct ccgcgcggc cgggcggggc gcgagggggc ggaggcgggg 2820

373 agcaggggag gcgcgtcggg ctgggaagtc gcgcgcacac tcggctccgg ggacagacgg 2880

375 ttaactcttg ccaagtctcg ccgcctctgc ggctcccggg ccttgggttt ccccttgaa 2940

377 gcatgagcct ttcttccgcg agccgcacac gctgcgcggg tctcggacag tgcgcgcgg 3000

379 gactccaggc gcgcgcctc aagatccctt gtgcccggag cccggaagct tgcggcaggt 3060

381 accgctcgcg aagccggaag gttccgccc gggggacagt ggccgggagg gcggcgggt 3120

383 gcgagcacgg gggcgggcgc ggaccgcctg ggcgtccgca gtttagggcg ccccgggaga 3180

385 gttcaagtcg gggctctgcc ccaccggac tcaactgcct cctctctccc gggttccttc 3240

387 tcggtctcgg gaaattttcc gagcaccccc acccccacac aactgctacc caaatttata 3300

389 atcctaataa cctgatctcc cgtctctccc cgcagcctc cgccttget cccccacccc 3360

391 accccttctc tttctcccat ctctcctcgt tcaactggag ggaaaccgg cactggcgag 3420

393 caggggtgtc agcctggggc ggagaggggg gggggaagct aggcgacgat ccctgggatt 3480

395 tttgtctgcc tttggcgcag aaaaactcgg ttgcttttac tgagcgcaga gccgattgca 3540

397 tccccaggca tctcttcca caataaacg taccggggg aactcagacg gacaccctc 3600

399 ctgccccct ggctcccccg ccccttgctc gctggggagg ctgcctagt cggaggcggc 3660

401 agtcgcggcg gtggaggtaa gacctcagtc ccagttgat gcattggccc ctgcgtctgc 3720

403 tgttgccggc tcagcccccg cctcatttg agctccggcg ggggtgcac gctccggccg 3780

405 attcctcgac agcgcgcgcg gcggcagccg caggagccgc ggtccgcgtt ttggagcgac 3840

407 cgcgcgtgag ccccccaccc tctctggag cgtgctccag gaagcggcag gagtgggggt 3900

409 gaggccgct ccgaggcagg gatgcagcg ctggcgcgcc gctagcgac cgcagacccc 3960

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa

VERIFICATION SUMMARY

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Input Set : A:\407T-923710US.txt

Output Set: N:\CRF3\03132002\I771208.raw

L:228 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:240 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:252 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:264 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:747 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:763 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:779 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:809 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:821 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:833 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
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L:881 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
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L:5395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:5439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:5469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:6659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:6661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:7101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:10033 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
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L:17465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:19205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:21047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:21055 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20